FastQC Report

Fri 15 Aug 2025
SRR33784444_2_paired.fastq

Summary

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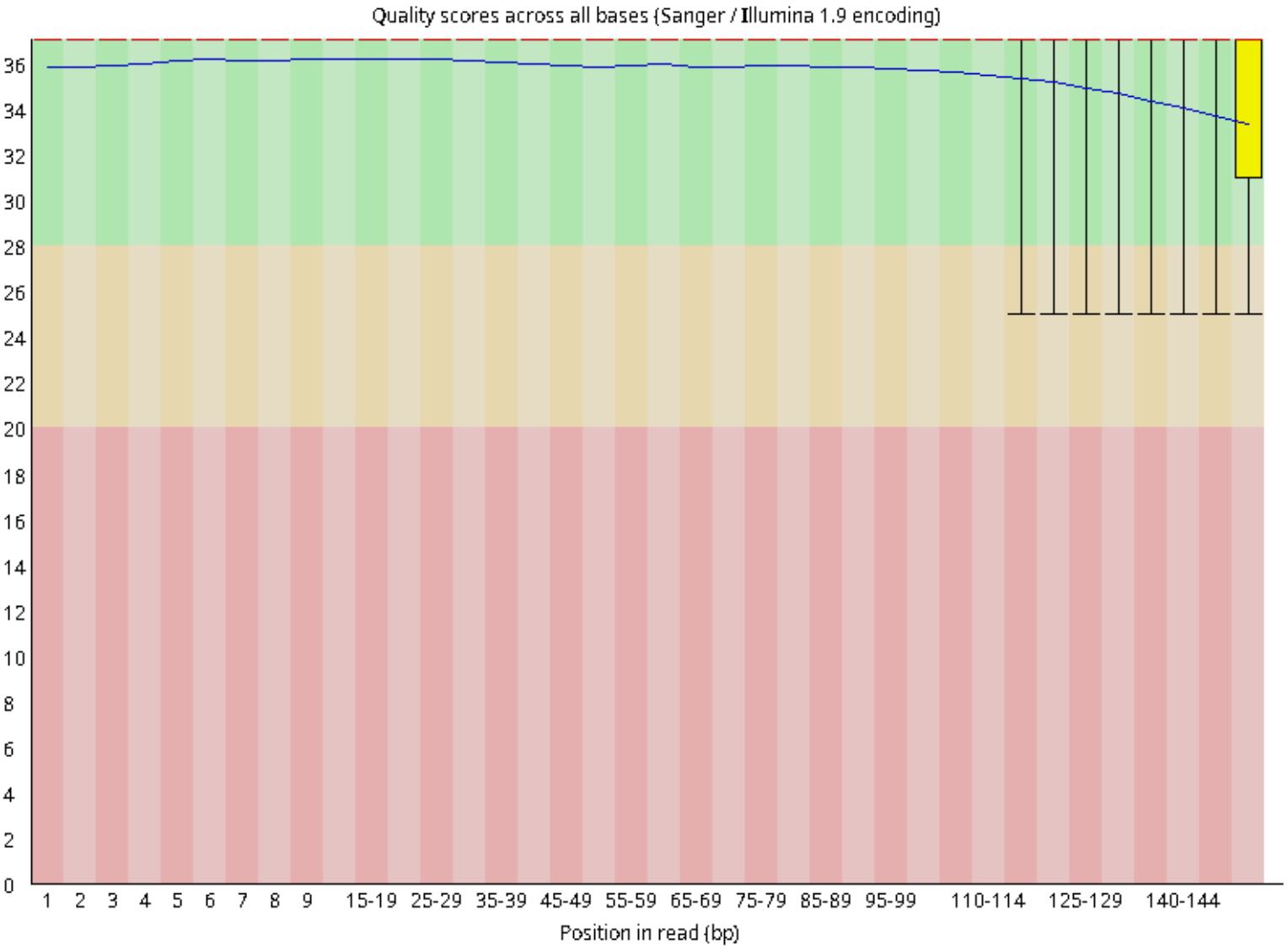
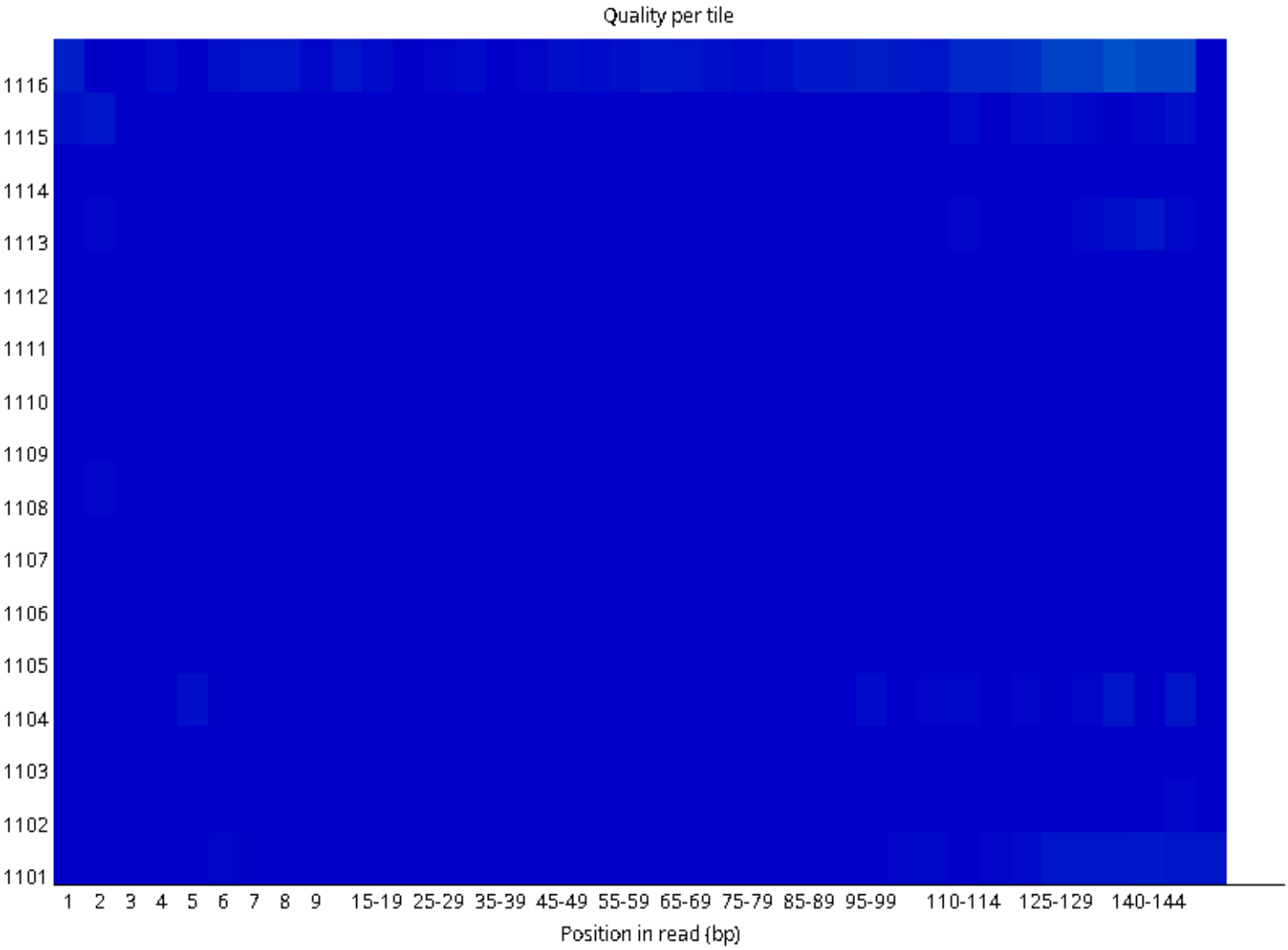
Basic Statistics

Measure	Value
Filename	SRR33784444_2_paired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	94421
Sequences flagged as poor quality	0
Sequence length	50-151
%GC	45

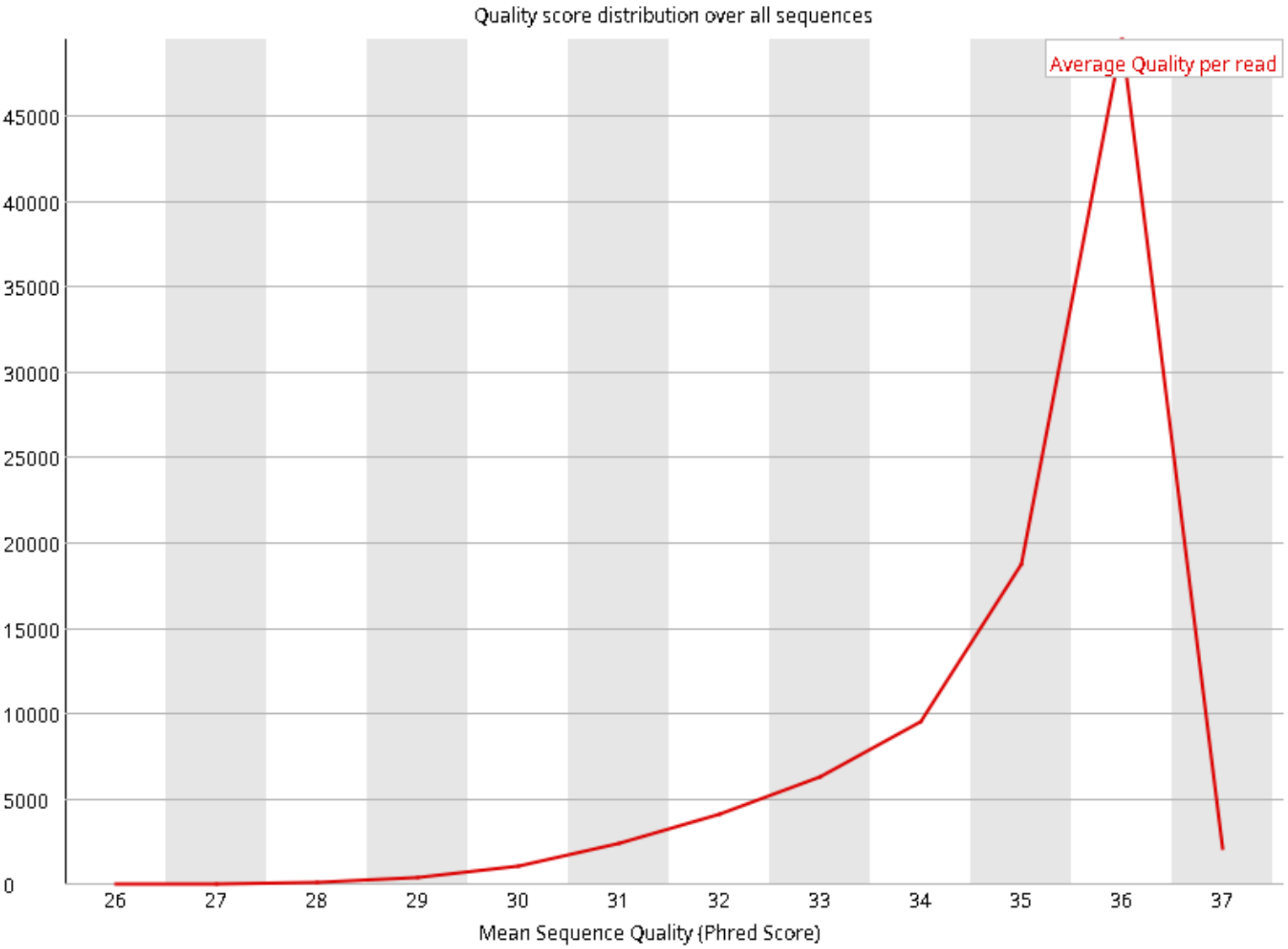
Per base sequence quality



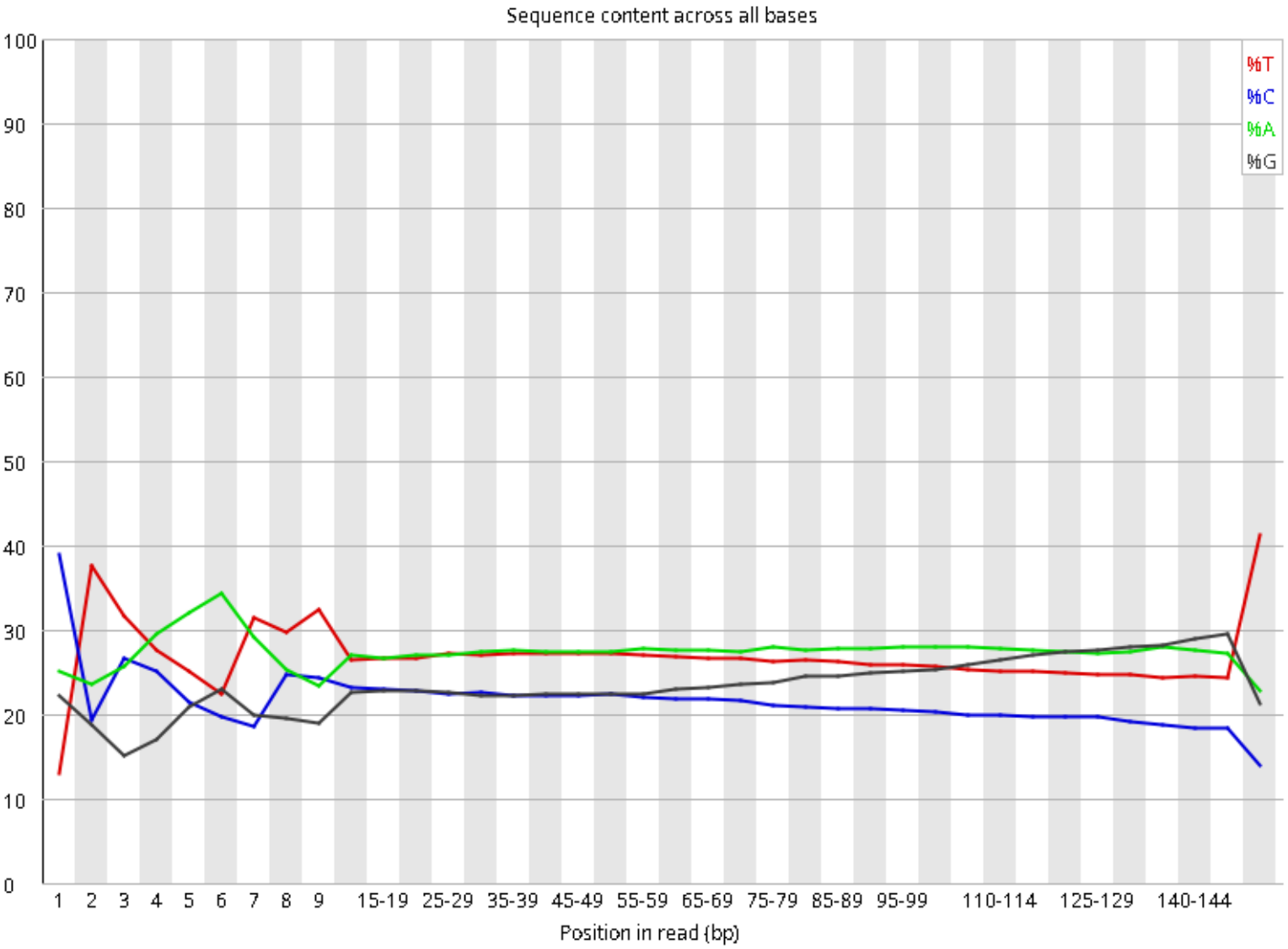
Per tile sequence quality



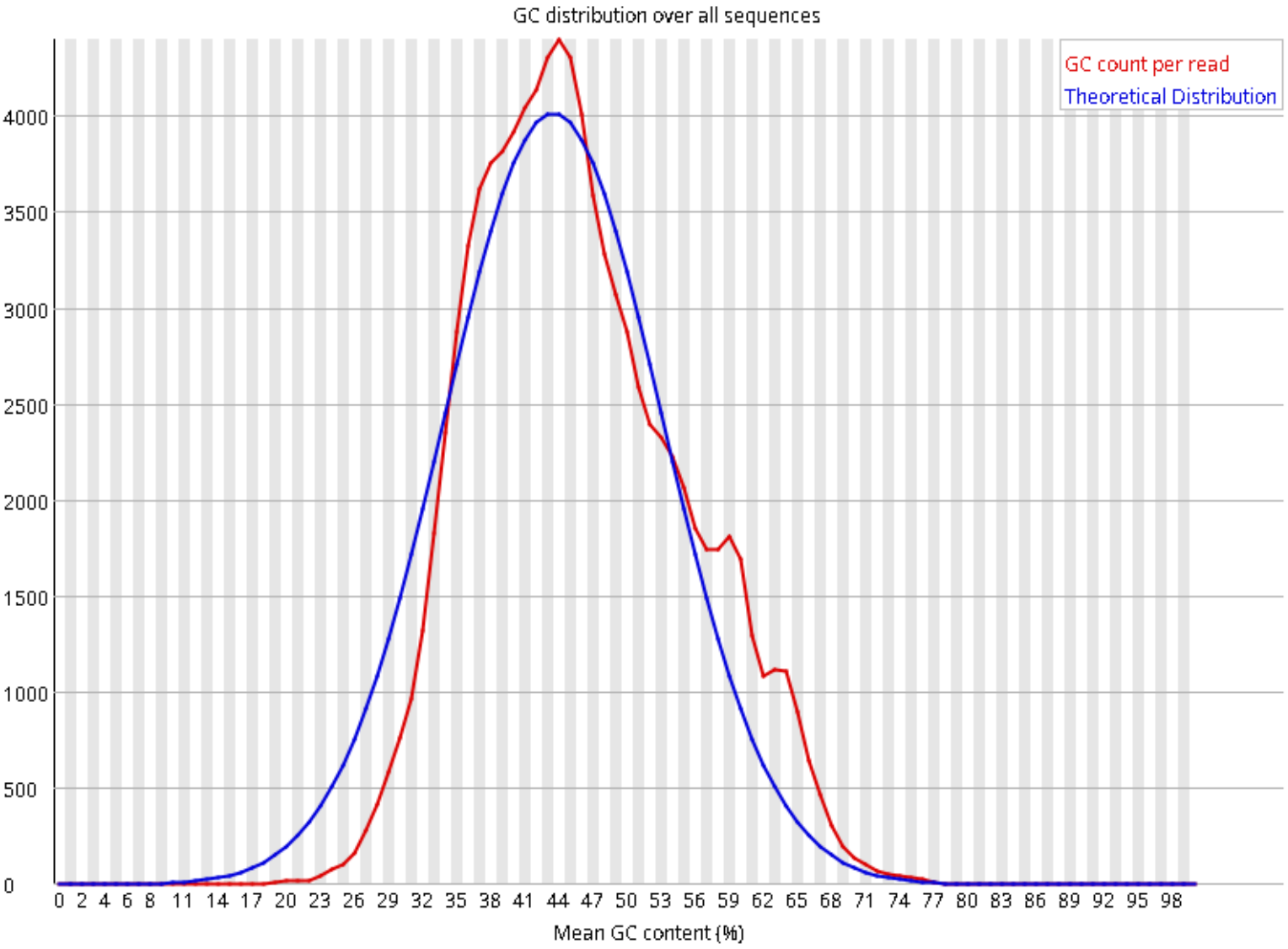
Per sequence quality scores



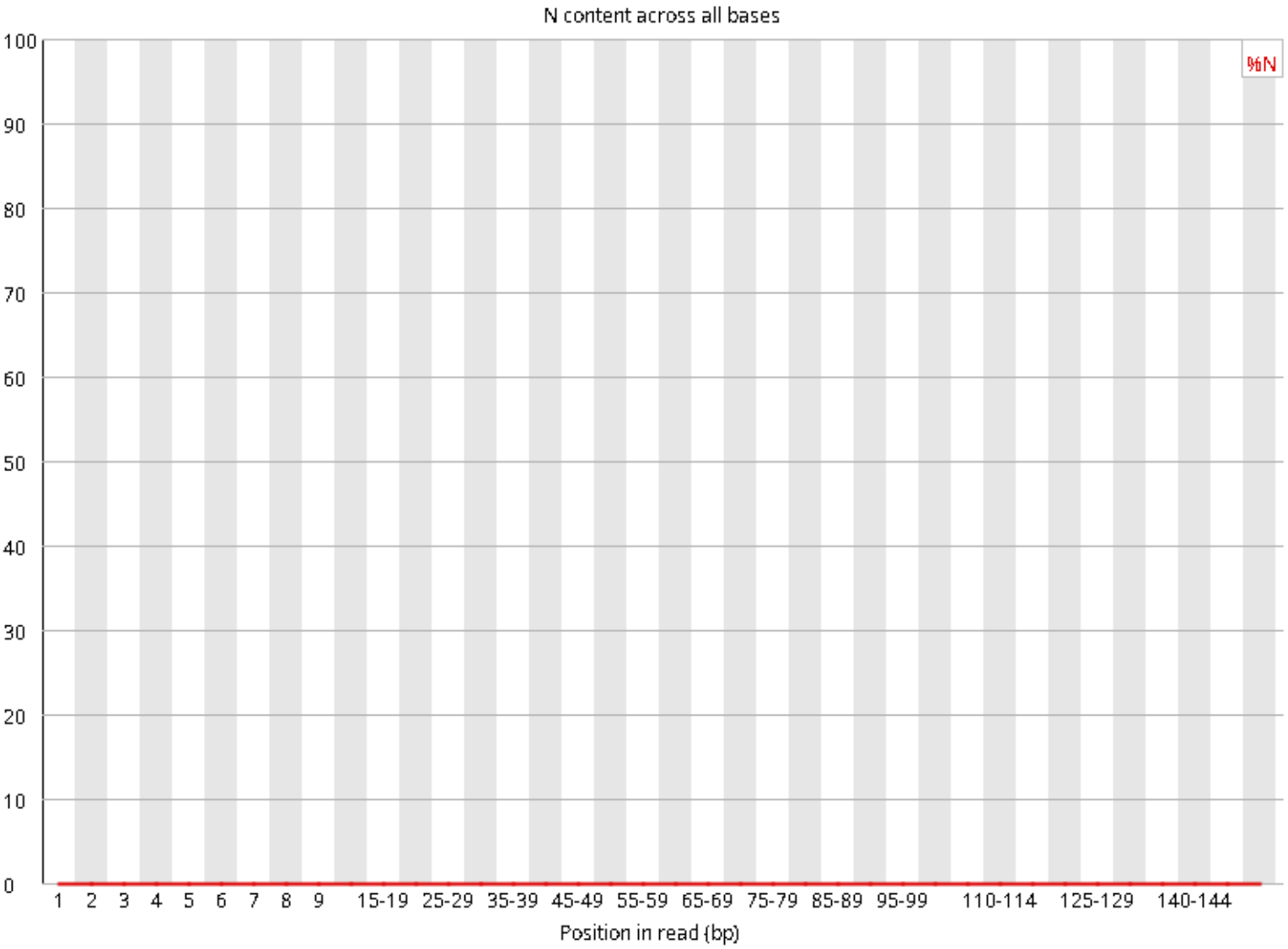
Per base sequence content



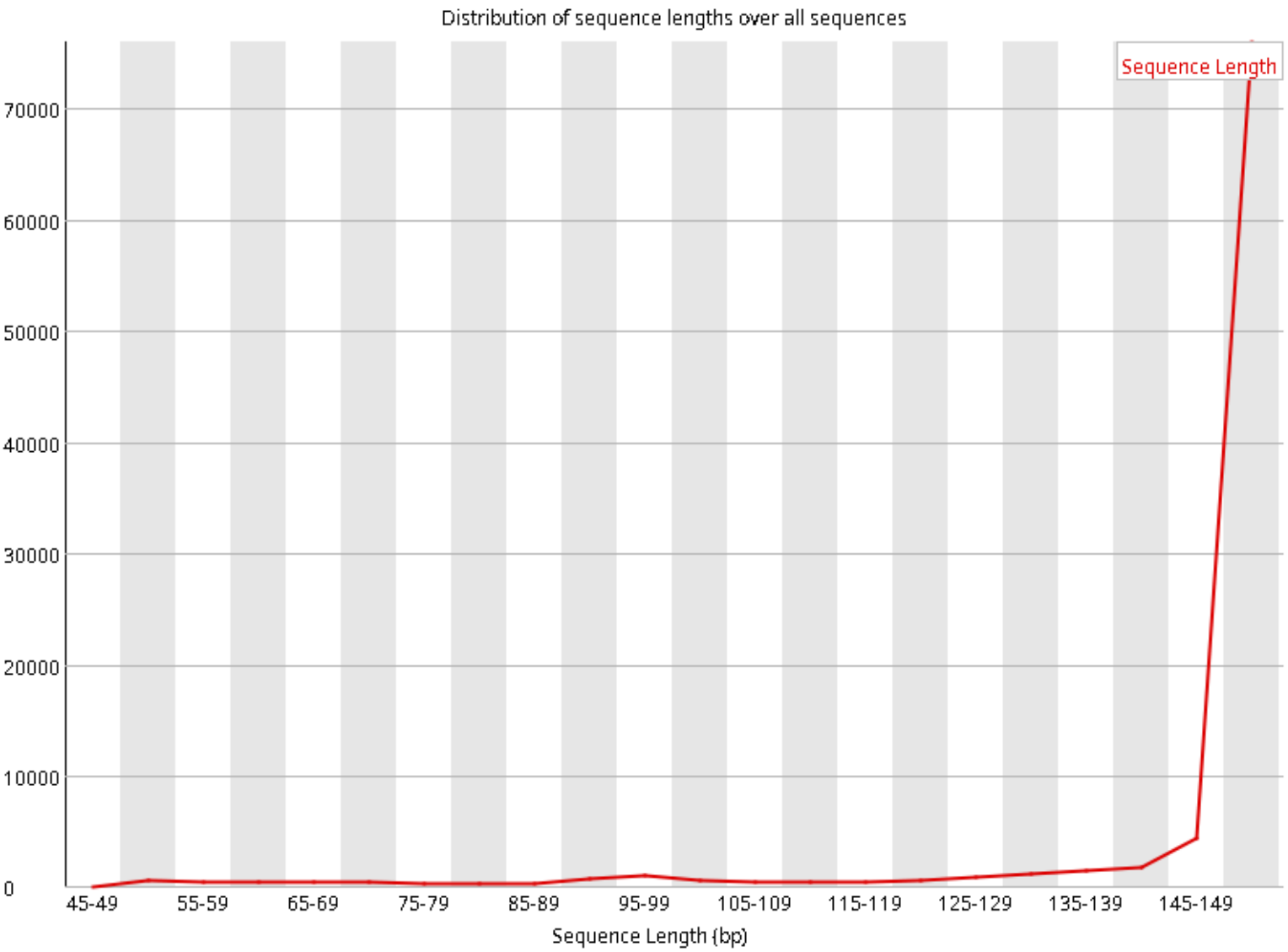
Per sequence GC content



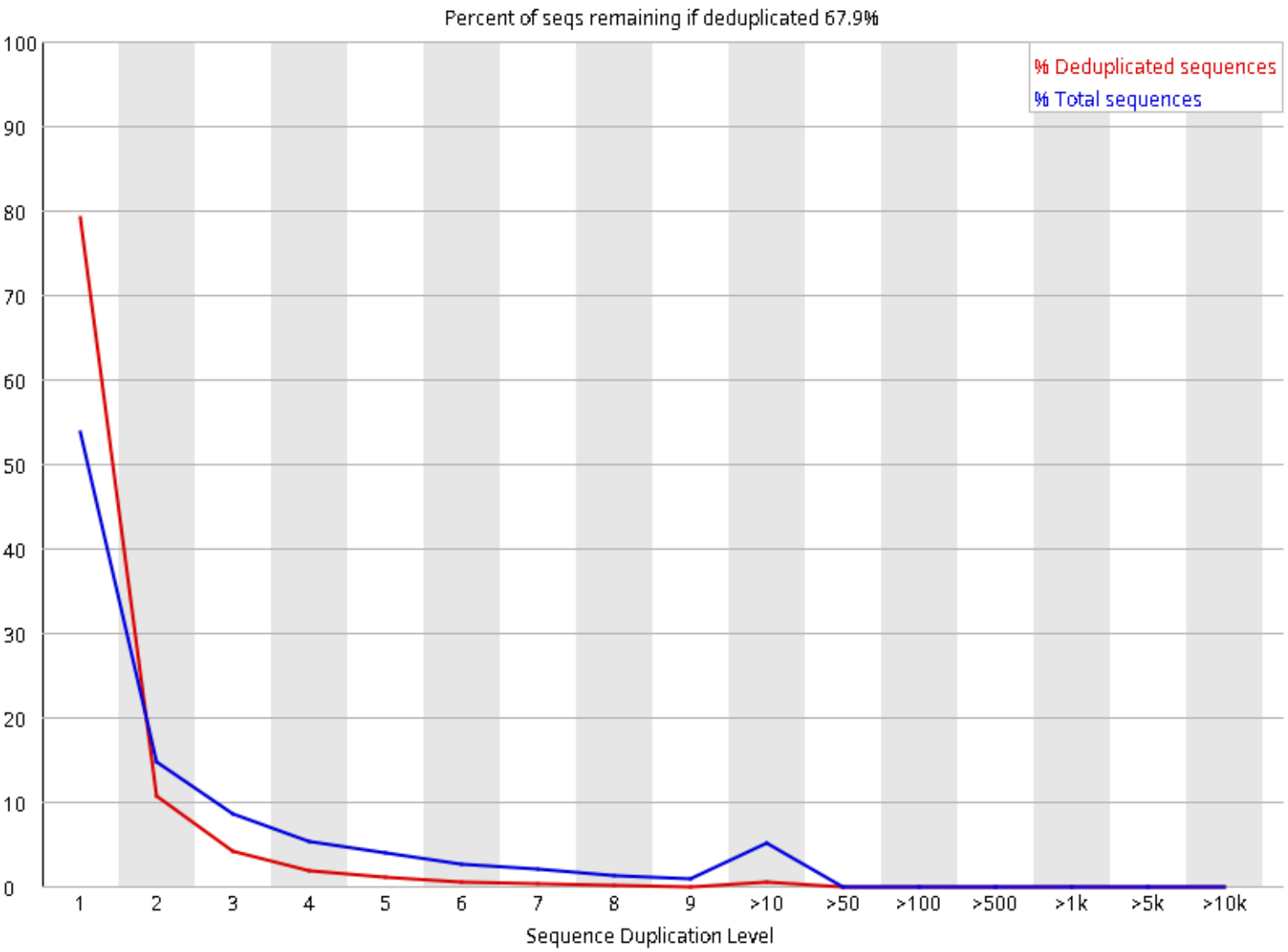
Per base N content



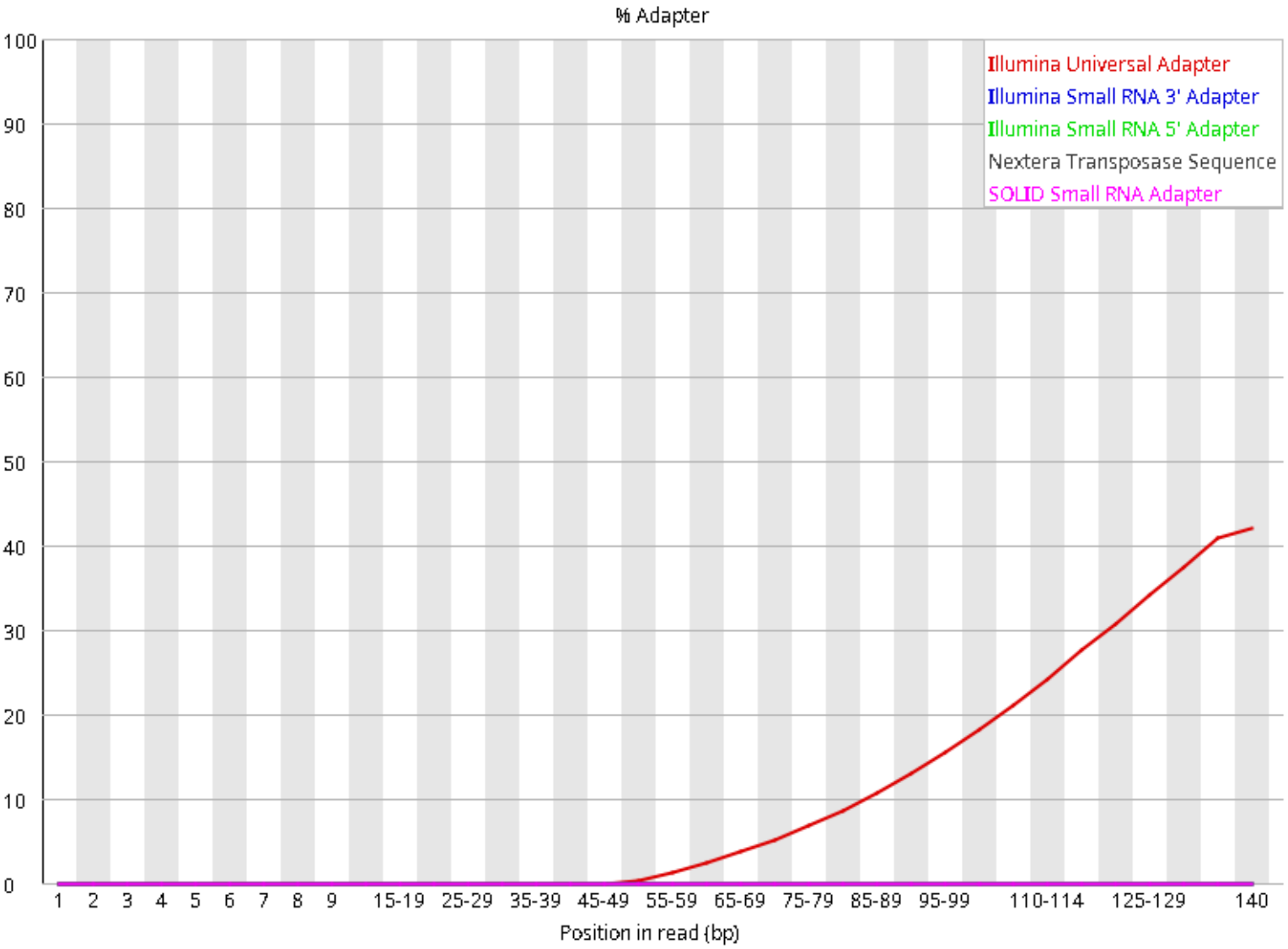
Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

No overrepresented sequences

Adapter Content